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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/879,959

DATE: 10/01/2001
 TIME: 10:39:26

Input Set : A:\PTO_VSK.txt
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3 <110> APPLICANT: Weigel, Paul H
 4 Kumari, Kshama
 5 DeAngelis, Paul
 7 <120> TITLE OF INVENTION: STREPTOCOCCUS EQUISIMILIS HYALURONAN SYNTHASE GENE AND
 EXPRESSION THEREOF

8 IN BACILLUS SUBTILIS
 10 <130> FILE REFERENCE: 3554.049
 12 <140> CURRENT APPLICATION NUMBER: US 09/879,959
 C--> 13 <141> CURRENT FILING DATE: 2001-09-12
 15 <150> PRIOR APPLICATION NUMBER: 09/469,200
 16 <151> PRIOR FILING DATE: 1999-12-21
 18 <150> PRIOR APPLICATION NUMBER: 09/178,851
 19 <151> PRIOR FILING DATE: 1998-10-26
 21 <160> NUMBER OF SEQ ID NOS: 10
 23 <170> SOFTWARE: PatentIn version 3.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1254
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Streptococcus equisimilis
 30 <400> SEQUENCE: 1

ENTERED

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33 atttacgtca atgtttatct ctttggtgct aaaggaagct tgtcaattta tggcttttttg      120
35 ctgatatgctt acctattagt caaaatgtcc ttatcctttt ttacaagcc atttaagggga      180
37 agggctgggc aatataaggt tgcagccatt attccctctt ataacgaaga tgctgagtc      240
39 ttgctagaga ccttaaaaag tggtcagcag caaacctatc ccctagcaga aatttatgtt      300
41 gttgacgatg gaagtgcga tgagacaggt attaagcgca ttgaagacta tgtgcgtgac      360
43 actggtgacc tatcaagcaa tgcattgtt gacgctgatg tctttttgac cgttgactca      420
45 catgcacagg cctgggcctt tgaaagatca gacgctgatg tctttttgac cgttgactca      480
47 gatacttata tctaccctga tgctttagag gagttgttaa aaacctttta tgaccaact      540
49 gtttttgctg cgacgggtca ccttaatgtc agaaatagac aaaccaatct cttaacacgc      600
51 ttgacagata ttcgctatga taatgctttt ggcgttgaac gagctgccca atccggttaca      660
53 ggtaatatcc ttgtttgctc aggtccgctt agcgtttaca gacgcgaggt ggttggttcc      720
55 aacatagata gatacatcaa ccagaccttc ctgggtattc ctgtaagtat tggatgatgac      780
57 aggtgcttga ccaactatgc aactgattta ggaaagactg tttatcaatc cactgctaaa      840
59 tgtattacag atgttcctga caagatgtct acttacttga agcagcaaaa ccgctggaac      900
61 aagtccttct ttagagagtc cattatttct gttaagaaaa tcatgaacaa tccttttgta      960
63 gccctatgga ccatacttga ggtgtctatg tttatgatgc ttgtttattc tgtggtggat      1020
65 ttctttgtag gcaatgtcag agaatttgat tggtcagggt ttttagcctt tctggtgatt      1080
67 atcttcattg ttgcctctgt tcggaacatt cattacatgc ttaagcacc cgtgtccttc      1140
69 ttgttatctc cgttttatgg ggtgctgcat ttgtttgtcc tacagccctt gaaattatat      1200
71 tctcttttta ctattagaaa tgctgactgg ggaacacgta aaaaattatt ataa      1254

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74 <210> SEQ ID NO: 2
 75 <211> LENGTH: 417
 76 <212> TYPE: PRT
 77 <213> ORGANISM: Streptococcus equisimilis
 79 <400> SEQUENCE: 2
 81 Met Arg Thr Leu Lys Asn Leu Ile Thr Val Val Ala Phe Ser Ile Phe
 82 1 5 10 15

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85 Trp Val Leu Leu Ile Tyr Val Asn Val Tyr Leu Phe Gly Ala Lys Gly
86          20          25          30
89 Ser Leu Ser Ile Tyr Gly Phe Leu Leu Ile Ala Tyr Leu Leu Val Lys
90          35          40          45
93 Met Ser Leu Ser Phe Phe Tyr Lys Pro Phe Lys Gly Arg Ala Gly Gln
94          50          55          60
97 Tyr Lys Val Ala Ala Ile Ile Pro Ser Tyr Asn Glu Asp Ala Glu Ser
98 65          70          75          80
101 Leu Leu Glu Thr Leu Lys Ser Val Gln Gln Gln Thr Tyr Pro Leu Ala
102          85          90          95
105 Glu Ile Tyr Val Val Asp Asp Gly Ser Ala Asp Glu Thr Gly Ile Lys
106          100          105          110
109 Arg Ile Glu Asp Tyr Val Arg Asp Thr Gly Asp Leu Ser Ser Asn Val
110          115          120          125
113 Ile Val His Arg Ser Glu Lys Asn Gln Gly Lys Arg His Ala Gln Ala
114          130          135          140
117 Trp Ala Phe Glu Arg Ser Asp Ala Asp Val Phe Leu Thr Val Asp Ser
118 145          150          155          160
121 Asp Thr Tyr Ile Tyr Pro Asp Ala Leu Glu Glu Leu Leu Lys Thr Phe
122          165          170          175
125 Asn Asp Pro Thr Val Phe Ala Ala Thr Gly His Leu Asn Val Arg Asn
126          180          185          190
129 Arg Gln Thr Asn Leu Leu Thr Arg Leu Thr Asp Ile Arg Tyr Asp Asn
130          195          200          205
133 Ala Phe Gly Val Glu Arg Ala Ala Gln Ser Val Thr Gly Asn Ile Leu
134          210          215          220
137 Val Cys Ser Gly Pro Leu Ser Val Tyr Arg Arg Glu Val Val Val Pro
138 225          230          235          240
141 Asn Ile Asp Arg Tyr Ile Asn Gln Thr Phe Leu Gly Ile Pro Val Ser
142          245          250          255
145 Ile Gly Asp Asp Arg Cys Leu Thr Asn Tyr Ala Thr Asp Leu Gly Lys
146          260          265          270
149 Thr Val Tyr Gln Ser Thr Ala Lys Cys Ile Thr Asp Val Pro Asp Lys
150          275          280          285
153 Met Ser Thr Tyr Leu Lys Gln Asn Arg Trp Asn Lys Ser Phe Phe
154          290          295          300
157 Arg Glu Ser Ile Ile Ser Val Lys Lys Ile Met Asn Asn Pro Phe Val
158 305          310          315          320
161 Ala Leu Trp Thr Ile Leu Glu Val Ser Met Phe Met Met Leu Val Tyr
162          325          330          335
165 Ser Val Val Asp Phe Phe Val Gly Asn Val Arg Glu Phe Asp Trp Leu
166          340          345          350
169 Arg Val Leu Ala Phe Leu Val Ile Ile Phe Ile Val Ala Leu Cys Arg
170          355          360          365
173 Asn Ile His Tyr Met Leu Lys His Pro Leu Ser Phe Leu Leu Ser Pro
174          370          375          380
177 Phe Tyr Gly Val Leu His Leu Phe Val Leu Gln Pro Leu Lys Leu Tyr
178 385          390          395          400
181 Ser Leu Phe Thr Ile Arg Asn Ala Asp Trp Gly Thr Arg Lys Lys Leu

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182          405          410          415
185 Leu
189 <210> SEQ ID NO: 3
190 <211> LENGTH: 22
191 <212> TYPE: DNA
192 <213> ORGANISM: Streptococcus equisimilis
194 <400> SEQUENCE: 3
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198 <210> SEQ ID NO: 4
199 <211> LENGTH: 20
200 <212> TYPE: DNA
201 <213> ORGANISM: Streptococcus equisimilis
203 <400> SEQUENCE: 4
204 atcaaattct ctgacattgc                20
207 <210> SEQ ID NO: 5
208 <211> LENGTH: 20
209 <212> TYPE: DNA
210 <213> ORGANISM: Streptococcus equisimilis
212 <400> SEQUENCE: 5
213 gactcagata cttatatcta                20
216 <210> SEQ ID NO: 6
217 <211> LENGTH: 17
218 <212> TYPE: DNA
219 <213> ORGANISM: Streptococcus equisimilis
221 <400> SEQUENCE: 6
222 tttttacgtg ttcccca                17
225 <210> SEQ ID NO: 7
226 <211> LENGTH: 567
227 <212> TYPE: PRT
228 <213> ORGANISM: Chlorella virus PBCV-1
230 <400> SEQUENCE: 7
232 Met Gly Lys Asn Ile Ile Ile Met Val Ser Trp Tyr Thr Ile Ile Thr
233 1          5          10          15
236 Ser Asn Leu Ile Ala Val Gly Gly Ala Ser Leu Ile Leu Ala Pro Ala
237          20          25          30
240 Ile Thr Gly Tyr Val Leu His Trp Asn Ile Ala Leu Ser Thr Ile Trp
241          35          40          45
244 Gly Val Ser Ala Tyr Gly Ile Phe Val Phe Gly Phe Phe Leu Ala Gln
245          50          55          60
248 Val Leu Phe Ser Glu Leu Asn Arg Lys Arg Leu Arg Lys Trp Ile Ser
249 65          70          75          80
252 Leu Arg Pro Lys Gly Trp Asn Asp Val Arg Leu Ala Val Ile Ile Ala
253          85          90          95
256 Gly Tyr Arg Glu Asp Pro Tyr Met Phe Gln Lys Cys Leu Glu Ser Val
257          100         105         110
260 Arg Asp Ser Asp Tyr Gly Asn Val Ala Arg Leu Ile Cys Val Ile Asp
261          115         120         125
264 Gly Asp Glu Asp Asp Asp Met Arg Met Ala Ala Val Tyr Lys Ala Ile
265          130         135         140

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268 Tyr Asn Asp Asn Ile Lys Lys Pro Glu Phe Val Leu Cys Glu Ser Asp
269 145 150 155 160
272 Asp Lys Glu Gly Glu Arg Ile Asp Ser Asp Phe Ser Arg Asp Ile Cys
273 165 170 175
276 Val Leu Gln Pro His Arg Gly Lys Arg Glu Cys Leu Tyr Thr Gly Phe
277 180 185 190
280 Gln Leu Ala Lys Met Asp Pro Ser Val Asn Ala Val Val Leu Ile Asp
281 195 200 205
284 Ser Asp Thr Val Leu Glu Lys Asp Ala Ile Leu Glu Val Val Tyr Pro
285 210 215 220
288 Leu Ala Cys Asp Pro Glu Ile Gln Ala Val Ala Gly Glu Cys Lys Ile
289 225 230 235 240
292 Trp Asn Thr Asp Thr Leu Leu Ser Leu Leu Val Ala Trp Arg Tyr Tyr
293 245 250 255
296 Ser Ala Phe Cys Val Glu Arg Ser Ala Gln Ser Phe Phe Arg Thr Val
297 260 265 270
300 Gln Cys Val Gly Gly Pro Leu Gly Ala Tyr Lys Asp Ile Ile Lys Glu
301 275 280 285
304 Ile Lys Asp Pro Trp Ile Ser Gln Arg Phe Leu Gly Gln Lys Cys Thr
305 290 295 300
308 Tyr Gly Asp Asp Arg Arg Leu Thr Asn Glu Ile Leu Met Arg Gly Lys
309 305 310 315 320
312 Lys Val Val Phe Thr Pro Phe Ala Val Gly Trp Ser Asp Ser Pro Thr
313 325 330 335
316 Asn Val Phe Arg Tyr Ile Val Gln Gln Thr Arg Trp Ser Lys Ser Trp
317 340 345 350
320 Cys Arg Glu Ile Trp Tyr Thr Leu Phe Ala Ala Trp Lys His Gly Leu
321 355 360 365
324 Ser Gly Ile Trp Leu Ala Phe Glu Cys Leu Tyr Gln Ile Thr Tyr Phe
325 370 375 380
328 Phe Leu Val Ile Tyr Leu Phe Ser Arg Leu Ala Val Glu Ala Asp Pro
329 385 390 395 400
332 Arg Ala Gln Thr Ala Thr Val Ile Val Ser Thr Thr Val Ala Leu Ile
333 405 410 415
336 Lys Cys Gly Tyr Phe Ser Phe Arg Ala Lys Asp Ile Arg Ala Phe Tyr
337 420 425 430
340 Phe Val Leu Tyr Thr Phe Val Tyr Phe Phe Cys Met Ile Pro Ala Arg
341 435 440 445
344 Ile Thr Ala Met Met Thr Leu Trp Asp Ile Gly Trp Asp Thr Arg Gly
345 450 455 460
348 Gly Asn Glu Lys Pro Ser Val Gly Thr Arg Val Ala Leu Trp Ala Lys
349 465 470 475 480
352 Gln Tyr Leu Ile Ala Tyr Met Trp Trp Ala Ala Val Val Gly Ala Gly
353 485 490 495
356 Val Tyr Ser Ile Val His Asn Trp Met Phe Asp Trp Asn Ser Leu Ser
357 500 505 510
360 Tyr Arg Phe Ala Leu Val Gly Ile Cys Ser Tyr Ile Val Phe Ile Val
361 515 520 525
364 Ile Val Leu Val Val Tyr Phe Thr Gly Lys Ile Thr Thr Trp Asn Phe

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365      530      535      540
368 Thr Lys Leu Gln Lys Glu Leu Ile Glu Asp Arg Val Leu Tyr Asp Ala
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373      565
376 <210> SEQ ID NO: 8
377 <211> LENGTH: 1740
378 <212> TYPE: DNA
379 <213> ORGANISM: Chlorella virus PBCV-1
381 <400> SEQUENCE: 8
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384 tcataacttc aaatctaata gcggttggag gagcctctct aatcttggct ccggcaatta      120
386 ctgggtatgt tctacattgg aatattgctc tctcgacaat ctggggagta tcagcttatg      180
388 gtattttcgt ttttgggttt ttcttgcac aagttttatt ttcagaactg aacaggaaac      240
390 gtcttcgcaa gtggatttct ctcagacctc agggttggaa tgatgttctg ttggctgtga      300
392 tcattgctgg atatcgcgag gatccttata tgttccagaa gtgcctcgag tctgtacgtg      360
394 actctgatta tggcaacgtt gcccgctctga tttgtgtgat tgacggtgat gaggacgatg      420
396 atatgaggat ggctgccgtt tacaaggcga tctacaatga taatatcaag aagcccgagt      480
398 ttgttctgtg tgagttagac gacaaggaag gtgaacgcat cgactctgat ttctctcgcg      540
400 acatttgtgt cctccagcct catcgtggaa aacgggagtg tctttatact gggtttcaac      600
402 ttgcaaagat ggacccagtg gtcaatgctg tcgttctgat tgacagcgat accgttctcg      660
404 agaaggatgc tattctggaa gttgtatacc cacttgcata cgatcccgag atccaagccg      720
406 ttgcaggtga gtgtaagatt tggaacacag acactctttt gactcttctc gtcgcttggc      780
408 ggtactatgc tgcgttttgt gtggagagga gtgccagtc ttttttcagg actgttcagt      840
410 gcgttggggg gccactgggt gctacaaga ttgatatcat taaggagatt aaggaccct      900
412 ggatttccca gcgctttctt ggtcagaagt gtacttacgg tgacgaccgc cggctaacca      960
414 acgagatctt gatgcgtggt aaaaagggtg tgttcaactc atttgcgtgt ggttggctctg      1020
416 acagtccgac caatgtgttt cggtagatcg ttcagcagac ccgctggagt aagtcgtggt      1080
418 gccgcgaaat ttggtacacc ctcttcgccc cgtggaagca cggtttgtct ggaatttggc      1140
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422 gcctagccgt tgaggccgac cctcgcgccc agacagccac ggtgattgtg agcaccacgg      1260
424 ttgcattgat taagtgtggg tatttttcat tccgagccaa ggatattcgg gcgttttact      1320
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428 tgacgctttg ggacattggc tgggatactc gcggtggaaa cgagaagcct tccgttggca      1440
430 cccgggtcgc tctgtgggca aagcaatata tcattgcata tatgtggtgg gccgcggttg      1500
432 ttggcgctgg agtttacagc atcgtccata actggatgtt cgattggaat tctctttctt      1560
434 atcgttttgc tttggttggt atttgttctt acattgtttt tattgttatt gtgctggtgg      1620
436 tttatttcac cggcaaaaatt acgacttgga atttcacgaa gcttcagaag gagctaatac      1680
438 aggatcgctg tctgtacgat gcaactacca atgctcagtc tgtgtgattt ttctgcaag      1740
441 <210> SEQ ID NO: 9
442 <211> LENGTH: 2937
443 <212> TYPE: DNA
444 <213> ORGANISM: pasteurilla multocida
446 <400> SEQUENCE: 9
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451 gttgaatttc aaattaccaa atgccaagaa aaactctcag cacatccttc tgttaattca      180
453 gcacatcttt ctgtaaataa agaagaaaaa gtcaatgttt gcgatagtcc gttagatatt      240
455 gcaacacaac tgttactttc caacgtaaaa aaattagtac tttctgactc ggaaaaaac      300

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date